Fig. 1a

```
GAATTCGCGG CCGCCTCTTG CGGTCCCAGA GTGGAGTGGA AGGTCTGGAG CTTTGGGAGG      60
AGACGGGGAG GACAGACTGG AGGCGTGTTC CTCCCGGATT TTCTTTTTCG TGCGAGCCCT     120
CGCGCGCGCG TACAGTCATC CCGCTGGTCT GACGATTGTG GAGAGGCGGT GGAGAGGCTT     180
CATCCATCCC ACCCGGTCGT CGCCGGGGAT TGGGGTCCCA GCGACACCTC CCCGGGAGAA     240
GCAGTGCCCA GGAAGTTTTC TGAAGCCGGG GAAGCTGTGC AGCCGAAGCC GCCGCCGCGC     300
CGGAGCCCGG GACACCGGCC ACCCTCCGCG CCACCCACCC TCGCTTTCTC CGGCTTCCTC     360
TGGCCCAGGC GCCGCGCGGA CCCGGCAGCT GTCTGCGCAC GCCGAGCTCC ACGGTGAAAA     420
AAAAAGTGAA GGTGTAAAAG CAGCACAAGT GCAATAAGAG ATATTTCCTC AAATTTGCCT     480
CAAG ATG GAA ACC CTT TGC CTC AGG GCA TCC TTT TGG CTG GCA CTG GTT       529
     Met Glu Thr Leu Cys Leu Arg Ala Ser Phe Trp Leu Ala Leu Val
     -20                 -15                 -10                      577
GGA TGT GTA ATC AGT GAT AAT CCT GAG AGA TAC AGC ACA AAT CTA AGC
Gly Cys Val Ile Ser Asp Asn Pro Glu Arg Tyr Ser Thr Asn Leu Ser
 -5              -1  1              5                  10
AAT CAT GTG GAT GAT TTC ACC ACT TTT CGT GGC ACA GAG CTC AGC TTC       625
Asn His Val Asp Asp Phe Thr Thr Phe Arg Gly Thr Glu Leu Ser Phe
            15                  20                  25
CTG GTT ACC ACT CAT CAA CCC ACT AAT TTG GTC CTA CCC AGC AAT GGC       673
Leu Val Thr Thr His Gln Pro Thr Asn Leu Val Leu Pro Ser Asn Gly
        30                  35                  40
TCA ATG CAC AAC TAT TGC CCA CAG CAG ACT AAA ATT ACT TCA GCT TTC       721
Ser Met His Asn Tyr Cys Pro Gln Gln Thr Lys Ile Thr Ser Ala Phe
    45                  50                  55
AAA TAC ATT AAC ACT GTG ATA TCT TGT ACT ATT TTC ATC GTG GGA ATG       769
Lys Tyr Ile Asn Thr Val Ile Ser Cys Thr Ile Phe Ile Val Gly Met
60                  65                  70                  75
```

Fig. 1b

```
GTG GGG AAT GCA ACT CTG CTC AGG ATC ATT TAC CAG AAC AAA TGT ATG      817
Val Gly Asn Ala Thr Leu Leu Arg Ile Ile Tyr Gln Asn Lys Cys Met
                  80                  85                  90
AGG AAT GGC CCC AAC GCG CTG ATA GCC AGT CTT GCC CTT GGA GAC CTT      865
Arg Asn Gly Pro Asn Ala Leu Ile Ala Ser Leu Ala Leu Gly Asp Leu
             95                 100                 105
ATC TAT GTG GTC ATT GAT CTC CCT ATC AAT GTA TTT AAG CTG CTG GCT      913
Ile Tyr Val Val Ile Asp Leu Pro Ile Asn Val Phe Lys Leu Leu Ala
        110                 115                 120
GGG CGC TGG CCT TTT GAT CAC AAT GAC TTT GGC GTA TTT CTT TGC AAG      961
Gly Arg Trp Pro Phe Asp His Asn Asp Phe Gly Val Phe Leu Cys Lys
    125                 130                 135
CTG TTC CCC TTT TTG CAG AAG TCC TCG GTG GGG ATC ACC GTC CTC AAC     1009
Leu Phe Pro Phe Leu Gln Lys Ser Ser Val Gly Ile Thr Val Leu Asn
140                 145                 150                 155
CTC TGC GCT CTT AGT GTT GAC AGG TAC AGA GCA GTT GCC TCC TGG AGT     1057
Leu Cys Ala Leu Ser Val Asp Arg Tyr Arg Ala Val Ala Ser Trp Ser
                160                 165                 170
CGT GTT CAG GGA ATT GGG ATT CCT TTG GTA ACT GCC ATT GAA ATT GTC     1105
Arg Val Gln Gly Ile Gly Ile Pro Leu Val Thr Ala Ile Glu Ile Val
            175                 180                 185
TCC ATC TGG ATC CTG TCC TTT ATC CTG GCC ATT CCT GAA GCG ATT GGC     1153
Ser Ile Trp Ile Leu Ser Phe Ile Leu Ala Ile Pro Glu Ala Ile Gly
        190                 195                 200
TTC GTC ATG GTA CCC TTT GAA TAT AGG GGT GAA CAG CAT AAA ACC TGT     1201
Phe Val Met Val Pro Phe Glu Tyr Arg Gly Glu Gln His Lys Thr Cys
    205                 210                 215
```

Fig. 1c

```
ATG CTC AAT GCC ACA TCA AAA TTC ATG GAG TTC TAC CAA GAT GTA AAG      1249
Met Leu Asn Ala Thr Ser Lys Phe Met Glu Phe Tyr Gln Asp Val Lys
220                 225                 230                 235
GAC TGG TGG CTC TTC GGG TTC TAT TTC TGT ATG CCC TTG GTG TGC ACT      1297
Asp Trp Trp Leu Phe Gly Phe Tyr Phe Cys Met Pro Leu Val Cys Thr
                240                 245                 250
GCG ATC TTC TAC ACC CTC ATG ACT TGT GAG ATG TTG AAC AGA AGG AAT      1345
Ala Ile Phe Tyr Thr Leu Met Thr Cys Glu Met Leu Asn Arg Arg Asn
            225                 260                 265
GGC AGC TTG AGA ATT GCC CTC AGT GAA CAT CTT AAG CAG CGT CGA GAA      1393
Gly Ser Leu Arg Ile Ala Leu Ser Glu His Leu Lys Gln Arg Arg Glu
        270                 275                 280
GTG GCA AAA ACA GTT TTC TGC TTG GTT GTA ATT TTT GCT CTT TGC TGG      1441
Val Ala Lys Thr Val Phe Cys Leu Val Val Ile Phe Ala Leu Cys Trp
    285                 290                 295
TTC CCT CTT CAC TTA AGC CGT ATA TTG AAG AAA ACT GTG TAT AAC GAA      1489
Phe Pro Leu His Leu Ser Arg Ile Leu Lys Lys Thr Val Tyr Asp Glu
300                 305                 310                 315
ATG GAC AAG AAC CGA TGT GAA TTA CTT AGT TTC TTA CTG CTC ATG GAT      1537
Met Asp Lys Asn Arg Cys Glu Leu Leu Ser Phe Leu Leu Leu Met Asp
                320                 325                 330
TAC ATC GGT ATT AAC TTG GCA ACC ATG AAT TCA TGT ATA AAC CCC ATA      1585
Tyr Ile Gyr Ile Asn Leu Ala Thr Met Asn Ser Cys Lie Asn Pro Ile
            335                 340                 345
GCT CTG TAT TTT GTG AGC AAG AAA TTT AAA AAT TGT TTC CAG TCA TGC      1633
Ala Leu Tyr Phe Val Ser Lys Lys Phe Lys Asn Cys Phe Gln Ser Cys
        350                 355                 360
```

Fig. 1d

```
CTC TGC TGC TGC TGT TAC CAG TCC AAA AGT CTG ATG ACC TCG GTC CCC      1681
Leu Cys Cys Cys Cys Tyr Gln Ser Lys Ser Leu Met Thr Ser Val Pro
    365                 370                 375
ATG AAC GGA ACA AGC ATC CAG TGG AAG AAC CAC GAT CAA AAC AAC CAC      1729
Met Asn Gly Thr Ser Ile Gln Trp Lys Asn His Asp Gln Asn Asn His
380                 385                 390                 395
AAC ACA GAC CGG AGC AGC CAT AAG GAC AGC ATG AAC TGACCACCCT           1775
Asn Thr Asp Arg Ser Ser His Lys Asp Ser Met Asn
                400                 405
TAGAAGCACT CCTCGGTACT CCCATAATCC TCTCGGAGAA AAAAATCACA AGGCAACTGT    1835
GACTCCGGGA ATCTCTTCTC TGATCCTTCT TCCTTAATTC ACTCCCACAC CCAAGAAGAA    1895
ATGCTTTCCA AAACCGCAAG GTAGACTGGT TTATCCACCC ACAACATCTA CGAATCGTAC    1955
TTCTTTAATT GATCTAATTT ACATATTCTG CGTGTTGTAT TCAGCACTAA AAAATGGTGG    2015
GAGCTGGGGG AGAATGAAGA CTGTTAAATG AAACCAGAAG GATATTTACT ACTTTTGCAT    2075
GAAAATAGAG CTTTCAAGTA CATGGCTAGC TTTTATGGCA GTTCTGGTGA ATGTTCAATG    2135
GGAACTGGTC ACCATGAAAC TTTAGAGATT AACGACAAGA TTTTCTACTT TTTTTAAGTG    2195
ATTTTTTGTC CTTCAGCCAA ACACAATATG GGCTCAGGTC ACTTTTATTT GAAATGTCAT    2255
TTGGTGCCAG TATTTTTTAA CTGCATAATA GCCTAACATG ATTATTTGAA CTTATTTACA    2315
CATAGTTTGA AAAAAAAAAG ACAAAAATAG TATTCAGGTG AGCAATTAGA TTAGTATTTT    2375
CCACGTCACT ATTTATTTTT TTAAAACACA AATTCTAAAG CTACAACAAA TACTACAGGC    2435
CCTTAAAGCA CAGTCTGATG ACACATTTGG CAGTTTAATA GATGTTACTC AAAGAATTTT    2495
TTAAGAACTG TATTTTATTT TTTAAATGGT GTTTTATTAC AAGGGACCTT GAACATGTTT    2555
TGTATGTTAA ATTCAAAAGT AATGCTTCAA TCAGATAGTT CTTTTTCACA AGTTCAATAC    2615
TGTTTTTCAT GTAAATTTTG TATGAAAAAT CAATGTCAAG TACCAAAATG TTAATGTATG    2675
TGTCATTTAA CTCTGCCTGA GACTTTCAGT GCACTGTATA TAGAAGTCTA AAACACACCT    2735
AAGAGAAAAA GATCGAATTT TTCAGATGAT TCGGAAATTT TCATTCAGGT ATTTGTAATA    2795
```

Fig. 1e

GTGACATATA TATGTATATA CATATCACCT CCTATTCTCT TAATTTTTGT TAAAATGTTA 2855
ACTGGCAGTA AGTCTTTTTT GATCATTCCC TTTTCCATAT AGGAAACATA ATTTTGAAGT 2915
GGCCAGATGA GTTTATCATG TCAGTGAAAA ATAATTACCC ACAAATGCCA CCAGTAACTT 2975
AACGATTCTT CACTTCTTGG GGTTTTCAGT ATGAACCTAA CTCCCCACCC CAACATCTCC 3035
CTCCCACATT GTCACCATTT CAAAGGGCCC ACAGTGACTT TTGCTGGGCA TTTTCCCAGA 3095
TGTTTACAGA CTGTGAGTAC AGCAGAAAAT CTTTTACTAC TGTGTGTGTG TATATATATA 3155
AACAATTGTA AATTTCTTTT AGCCCATTTT TCTAGACTGT CTCTGTGGAA TATATTTGTG 3215
TGTGTGATAT ATGCATGTGT GTGATGGTAT GTATGGATTT AATCTAATCT AATAATTGTG 3275
CCCCGCAGTT GTGCCAAAGT GCATAGTCTG AGCTAAAATC TAGGTGATTG TTCATCATGA 3335
CACCCTGCCT CAGTCCATTT TAACCTGTAG CAACCTTCTG CATTCATAAA TCTTGTAATC 3395
ATGTTACCAT TACAAATGGG ATATAAGAGG CAGCGTGAAA GCAGATGAGC TGTGGACTAG 3455
CAATATAGGG TTTTGTTTGG TTGGTTGGTT TGATAAAGCA GTATTTGGGG TCATATTGTT 3515
TCCTGTGCTG GAGCAAAAGT CATTACACTT TGAAGTATTA TATTGTTCTT ATCCTCAATT 3575
CAATGTGGTG ATGAAATTGC CAGGTTGTCT GATATTTCTT TCAGACTTCG CCAGACAGAT 3635
TGCTGATAAT AAATTAGGTA AGATAATTTG TTGGGCCATA TTTTAGGACA GGTAAAATAA 3695
CATCAGGTTC CAGTTGCTTG AATTGCAAGG CTAAGAAGTA CTGCCCTTTT GTGTGTTAGC 3755
AGTCAAATCT ATTATTCCAC TGGCGCATCA TATGCAGTGA TATATGCCTA TAATATAAGC 3815
CATAGGTTCA CACCATTTTG TTTAGACAAT TGTCTTTTTT TCAAGATGCT TTGTTTCTTT 3875
CATATGAAAA AAATGCATTT TATAAATTCA GAAAGTCATA GATTTCTGAA GGCGTCAACG 3935
TGCATTTTAT TTATGGACTG GTAAGTAACT GTGGTTTACT AGCAGGAATA TTTCCAATTT 3995
CTACCTTTAC TACATCTTTT CAACAAGTAA CTTTGTAGAA ATGAGCCAGA AGCCAAGGCC 4055
CTGAGTTGGC AGTGGCCCAT AAGTGTAAAA TAAAAGTTTA CAGAAACCTT 4105

Fig. 2a

```
GAGACATTCC GGTGGGGGAC TCTGGCCAGC CCGAGCAACG TGGATCCTGA GAGCACTCCC      60
AGGTAGGCAT TTGCCCCGGT GGGACGCCTT GCCAGACCAG TGTGTGGCAG GCCCCCGTGG     120
AGGATCAACA CAGTGGCTGA ACACTGGGAA GGAACTGGTA CTTGGAGTCT GGACATCTGA     180
AACTTGGCTC TGAAACTGCG GAGCGGCCAC CGGACGCCTT CTGGAGCAGG TAGCAGC        237
ATG CAG CCG CCT CCA AGT CTG TGC GGA CGC GCC CTG GTT GCG CTG GTT        285
Met Gln Pro Pro Pro Ser Leu Cys Gly Arg Ala Leu Val Ala Leu Val
 1               5                  10                  15
CTT GCC TGC GGC CTG TCG CGG ATC TGG GGA GAG GAG AGA GGC TTC CCG       333
Leu Ala Cys Gly Leu Ser Arg Ile Trp Gly Glu Glu Arg Gly Phe Pro
            20                  25                  30
CCT GAC AGG GCC ACT CCG CTT TTG CAA ACC GCA GAG ATA ATG ACG CCA       381
Pro Asp Arg Ala Thr Pro Leu Leu Gln Thr Ala Glu Ile Met Thr Pro
        35                  40                  45
CCC ACT AAG ACC TTA TGG CCC AAG GGT TCC AAC GCC AGT CTG GCG CGG       429
Pro Thr Lys Thr Leu Trp Pro Lys Gly Ser Asn Ala Ser Leu Ala Arg
    50                  55                  60
TCG TTG GCA CCT GCG GAG GTG CCT AAA GGA GAC AGG ACG GCA GGA TCT       477
Ser Leu Ala Pro Ala Glu Val Pro Lys Gly Asp Arg Thr Ala Gly Ser
65                  70                  75                  80
CCG CCA CGC ACC ATC TCC CCT CCC CCG TGC CAA GGA CCC ATC GAG ATC       525
Pro Pro Arg Thr Ile Ser Pro Pro Pro Cys Gln Gly Pro Ile Glu Ile
                85                  90                  95
AAG GAG ACT TTC AAA TAC ATC AAC ACG CTT GTG TCC TGC CTT GTG TTC       573
Lys Glu Thr Phe Lys Tyr Ile Asn Thr Val Val Ser Cys Leu Val Phe
            100                 105                 110
```

Fig. 2b

```
GTG CTG GGG ATC ATC GGG AAC TCC ACA CTT CTG AGA ATT ATC TAC AAG      621
Val Leu Gly Ile Ile Gly Asn Ser Thr Leu Leu Arg Ile Ile Tyr Lrs
        115                 120                 125
AAC AAG TGC ATG CGA AAC GGT CCC AAT ATC TTG ATC GCC AGC TTG GCT      669
Asn Lys Gys Met Arg Asn Gly Pro Asn Ile Leu Ile Ala Ser Leu Ala
    130                 135                 140
CTG GGA GAC CTG CTG CAC ATC GTC ATT GAC ATC CCT ATC AAT GTC TAC      717
Leu Gly Asp Leu Leu His Ile Val Ile Asp Ile Pro Ile Asn Val Tyr
145                 150                 155                 160
AAG CTG CTG GCA GAG GAC TGG CCA TTT GGA GCT GAG ATG TGT AAG CTG      765
Lys Leu Leu Ala Glu Asp Trp Pro Phe Gly Ala Glu Met Cys Lys Leu
                165                 170                 175
GTG CCT TTC ATA CAG AAA GCC TCC GTG GGA ATC ACT GTG CTG AGT CTA      813
Val Pro Phe Ile Gln Lys Ala Ser Val Gly Ile Thr Val Leu Ser Leu
            180                 185                 190
TGT GCT CTG AGT ATT GAC AGA TAT CGA GCT GTT GCT TCT TGG AGT AGA      861
Cys Ala Leu Ser Ile Asp Arg Tyr Arg Ala Val Ala Ser Trp Ser Arg
        195                 200                 205
ATT AAA GGA ATT GGG GTT CCA AAA TGG ACA GCA GTA GAA ATT GTT TTG      909
Ile Lys Gly Ile Gly Val Pro Lys Trp Thr Ala Val Glu Ile Val Leu
    210                 215                 220
ATT TGG GTG GTC TCT GTG GTT CTG GCT GTC CCT GAA GCC ATA GGT TTT      957
Ile Trp Val Val Ser Val Val Leu Ala Val Pro Glu Ala Ile Gly Phe
225                 230                 235                 240
GAT ATA ATT ACG ATG GAC TAC AAA GGA AGT TAT CTG CGA ATC TGC TTG      1005
Asp Ile Ile Thr Met Asp Tyr Lys Gly Ser Tyr Leu Arg Ile Cys Leu
                245                 250                 255
```

Fig. 2c

```
CTT CAT CCC GTT CAG AAG ACA GCT TTC ATG CAG TTT TAC AAG ACA GCA      1053
Leu His Pro Val Gln Lys Thr Ala Phe Met Gln Phe Tyr Lys Thr Ala
            260                 265                 270
AAA GAT TGG TGG CTG TTC AGT TTC TAT TTC TGC TTG CCA TTG GCC ATC      1101
Lys Asp Typ Trp Leu Phe Ser Phe Tyr Phe Cys Leu Pro Leu Ala Ile
        275                 280                 285
ACT GCA TTT TTT TAT ACA CTA ATG ACC TGT GAA ATG TTG AGA AAG AAA      1149
Thr Ala Phe Phe Tyr Thr Leu Met Thr Cys Glu Met Leu Arg Lys Lys
    290                 295                 300
AGT GGC ATG CAG ATT GCT TTA AAT GAT CAC CTA AAG CAG AGA CGG GAA      1197
Ser Gly Met Gln Ile Ala Leu Asn Asp His Leu Lys Gln Arg Arg Glu
305                 310                 315                 320
GTG GCC AAA ACC GTC TTT TGC CTG GTC CTT GTC TTT GCC CTC TGC TGG      1245
Val Ala Lys Thr Val Phe Cys Leu Val Leu Val Phe Ala Leu Cys Trp
                325                 330                 335
CTT CCC CTT CAC CTC AGC AGG ATT CTG AAG CTC ACT GTT TAT AAT CAG      1293
Leu Pro Leu His Leu Ser Arg Ile Leu Lys Leu Thr Leu Tyr Asp Gln
            340                 345                 350
AAT GAT CCC AAT AGA TGT GAA CTT TTG AGC TTT CTG TTG GTA TTG GAC      1341
Asn Asp Pro Asn Arg Cys Glu Leu Leu Ser Phe Leu Leu Val Leu Asp
        355                 360                 365
TAT ATT GGT ATG AAC ATG GCT TCA CTG AAT TCC TGC ATT AAC CCA ATT      1389
Tyr Ile Gyr Ile Asn Met Ala Ser Leu Asn Ser Cys Ile Asn Pro Ile
    370                 375                 380
GCT CTG TAT TTC GTG AGC AAA AGA TTC AAA AAC TGC TTT AAG TCA TGC      1437
Ala Leu Tyr Leu Val Ser Lys Arg Phe Lys Asn Cys Phe Lys Ser Cys
385                 390                 395                 400
```

Fig. 2d

```
TTA TGC TGC TGG TGC CAG TCA TTT GAA GAA AAA CAG TCC TTG GAG GAA      1485
Leu Cys Cys Trp Cys Gln Ser Phe Glu Glu Lys Gln Ser Leu Glu Glu
                405                 410                 415
AAG CAG TCG TGC TTA AAG TTC AAA GCT AAT GAT CAC GGA TAT GAC AAC      1533
Lys Gln Ser Cys Leu Lys Phe Lys Ala Asn Asp His Gly Tyr Asp Asn
            420                 425                 430
TTC CGT TCC AGT AAT AAA TAC AGC TCA TCT TGAAAGAAGA ACTATTCACT        1583
Phe Arg Ser Ser Asn Lys Tyr Ser Ser Ser
        435                 440
GTATTTCATT TTCTTTATAT TGGACGGAAG TCATTAAAAC AAAATGAAAC ATTTGCCAAA    1643
ACAAAACAAA AAACTATGTA TTTGCACAGC ACACTATTAA AATATTAAGT GTAATTATTT    1703
TAACACTCAC AGCTACATAT GACATTTTAT GAGCTGTTTA CGGCATGGAA AGAAAATCAG    1763
AGGGAATTAA GAAAGCCTCG TCGTGAAAGC ACTTAATTTT TTACAGTTAG CACTTCAACA    1823
TAGCTCTTAA CAACTTCCAG GATATTCACA CAACACTTAG GCTTAAAAAT GAGCTCACTC    1883
AGAATTTCTA TTCTTTCTAA AAAGAGATTT ATTTTTAAAT CAATGGGACT CTGATATAAA    1943
GGAAGAATAA GTCACTGTAA AACAGAACTT TTAAATGAAG CTTAAATTAC TCAATTTAAA    2003
ATTTTAAAAT CCTTTAAAAC AACTTTTCAA TTAATATTAT CACACTATTA TCAGATTGTA    2063
ATTAGATGCA AATGAGAGAG CAGTTTAGTT GTTGCATTTT TCGGACACTG GAAAGATTTA    2123
AATGATCAGG AGGGAGTAAC AGAAAGAGCA AGGCTGTTTT TGAAATTCAT TACACTTTCA    2183
CTAGAAGCCC AAACCTCAGC ATTCTGCAAT ATGTAACCAA CATGTCACAA ACAAGCAGCA    2243
TGTAACAGAC TGGCACATGT GCCAGCTGAA TTTAAAATAT AATACTTTTA AAAAGAAAAT    2303
TATTACATCC TTTACATTCA GTTAAGATCA AACCTCACAA AGAGAAATAG AATGTTTGAA    2363
AGGCTATCCC AAAAGACTTT TTTGAATCTG TCATTCACAT ACCCTGTGAA GACAATACTA    2423
TCTACAATTT TTTCAGGATT ATTAAAATCT TCTTTTTTCA CTATCGTAGC TTAAACTCTG    2483
TTTGGTTTTG TCATCTGTAA ATACTTACCT ACATACACTG CATGTAGATG ATTAAATGAG    2543
GGCAGGCCCT GTGCTCATAG CTTTACGATG GAGAGATGCC AGTGACCTCA TAATAAAGAC    2603
TGTGAACTGC CTGGTGCAGT GTCCACATGA CAAAGGGGCA GGTAGCACCC TCTCTCACCC    2663
```

Fig. 2e


```
ATGCTGTGGT TAAAATGGTT TCTAGCATAT GTATAATGCT ATAGTTAAAA TACTATTTTT   2723
CAAAATCATA CAGATTAGTA CATTTAACAG CTACCTGTAA AGCTTATTAC TAATTTTTGT   2783
ATTATTTTTG TAAATAGCCA ATAGAAAAGT TTGCTTGACA TGGTGCTTTT CTTTCATCTA   2843
GAGGCAAAAC TGCTTTTTGA GACCGTAAGA ACCTCTTAGC TTTGTGCGTT CCTGCCTAAT   2903
TTTTATATCT TCTAAGCAAA GTGCCTTAGG ATAGCTTGGG ATGAGATGTG TGTGAAAGTA   2963
TGTACAAGAG AAAACGGAAG AGAGAGGAAA TGAGGTGGGG TTGGAGGAAA CCCATGGGGA   3023
CAGATTCCCA TTCTTAGCCT AACGTTCGTC ATTGCCTCGT CACATCAATG CAAAAGGTCC   3083
TGATTTTGTT CCAGCAAAAC ACAGTGCAAT GTTCTCAGAG TGACTTTCGA AATAAATTGG   3143
GCCCAAGAGC TTTAACTCGG TCTTAAAATA TGCCCAAATT TTTACTTTGT TTTTCTTTTA   3203
ATAGGCTGGG CCACATGTTG GAAATAAGCT AGTAATGTTG TTTTCTGTCA ATATTGAATG   3263
TGATGGTACA GTAAACCAAA ACCCAACAAT GTGGCCAGAA AGAAAGAGCA ATAATAATTA   3323
ATTCACACAC CATATGGATT CTATTTATAA ATCACCCACA AACTTGTTCT TTAATTTCAT   3383
CCCAATCACT TTTTCAGAGG CCTGTTATCA TAGAAGTCAT TTTAGACTCT CAATTTTAAA   3443
TTAATTTTGA ATCACTAATA TTTTCACAGT TTATTAATAT ATTTAATTTC TATTTAAATT   3503
TTAGATTATT TTTATTACCA TGTACTGAAT TTTTACATCC TGATACCCTT TCCTTCTCCA   3563
TGTCAGTATC ATGTTCTCTA ATTATCTTGC CAAATTTTGA AACTACACAC AAAAAGCATA   3623
CTTGCATTAT TTATAATAAA ATTGCATTCA GTGGCTTTTT AAAAAAAATG TTTGATTCAA   3683
AACTTTAACA TACTGATAAG TAAGAAACAA TTATAATTTC TTTACATACT CAAAACCAAG   3743
ATAGAAAAAG GTGCTATCGT TCAACTTCAA AACATGTTTC CTAGTATTAA GGACTTTAAT   3803
ATAGCAACAG ACAAAATTAT TGTTAACATG GATGTTACAG CTCAAAAGAT TTATAAAAGA   3863
TTTTAACCTA TTTTCTCCCT TATTATCCAC TGCTAATGTG GATGTATGTT CAAACACCTT   3923
TTAGTATTGA TAGCTTACAT ATGGCCAAAG GAATACAGTT TATAGCAAAA CATGGGTATG   3983
CTGTAGCTAA CTTTATAAAA GTGTAATATA ACAATGTAAA AAATTATATA TCTGGGAGGA   4043
TTTTTTGGTT GCCTAAAGTG GCTATAGTTA CTGATTTTTT ATTATGTAAG CAAAACCAAT   4103
AAAAATTTAA GTTTTTTTAA CAACTACCTT ATTTTTCACT GTACAGACAC TAATTCATTA   4163
AATACTAATT GATTGTTTAA AAGAAATATA AATGTGACAA GTGGACATTA TTTATGTTAA   4223
ATATACAATT ATCAAGCAAG TATGAAGTTA TTCAATTAAA ATGCCACATT TCTGGTCTCT   4283
GGGAAAAAAA AAAAAAAA                                                 4301
```

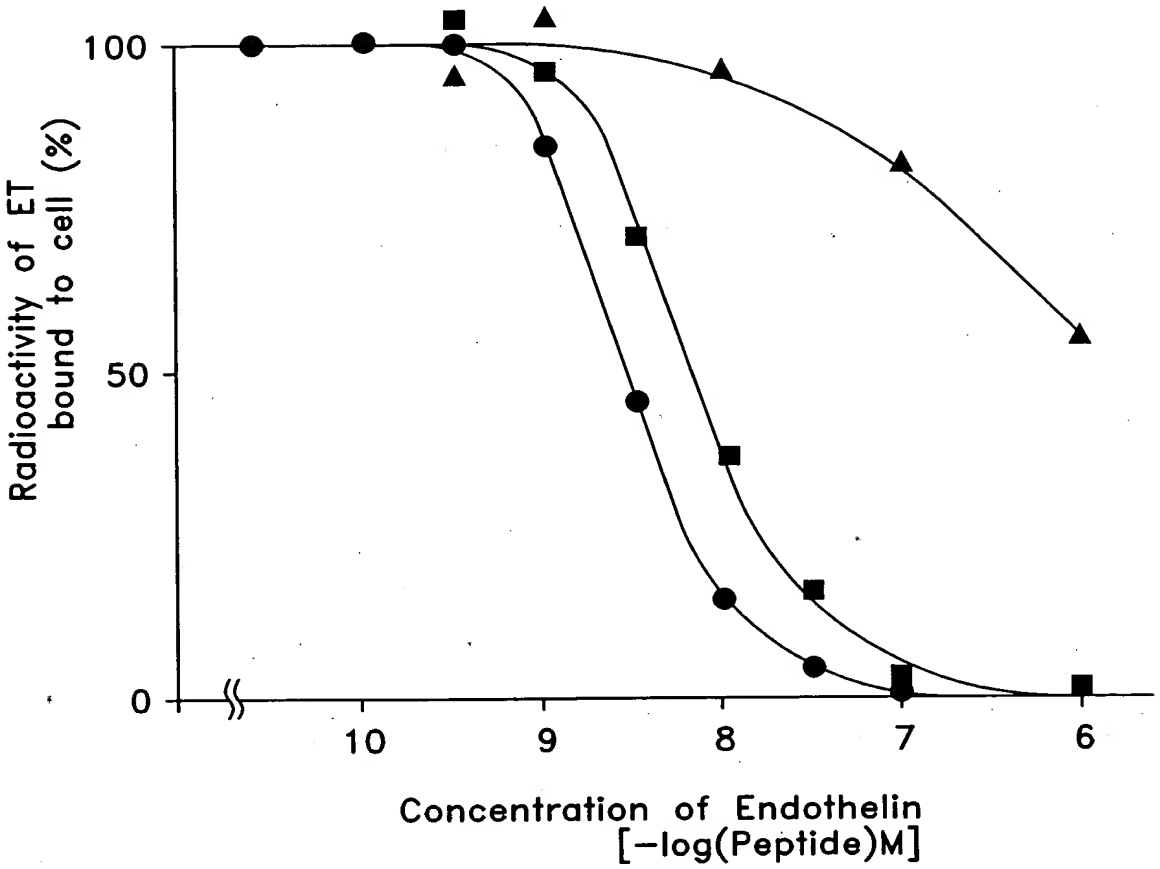
100
50
0
Radioactivity of ET bound to cell (%)
10
9
8
7
6
Concentration of Endothelin
[−log(Peptide)M]

Fig. 3

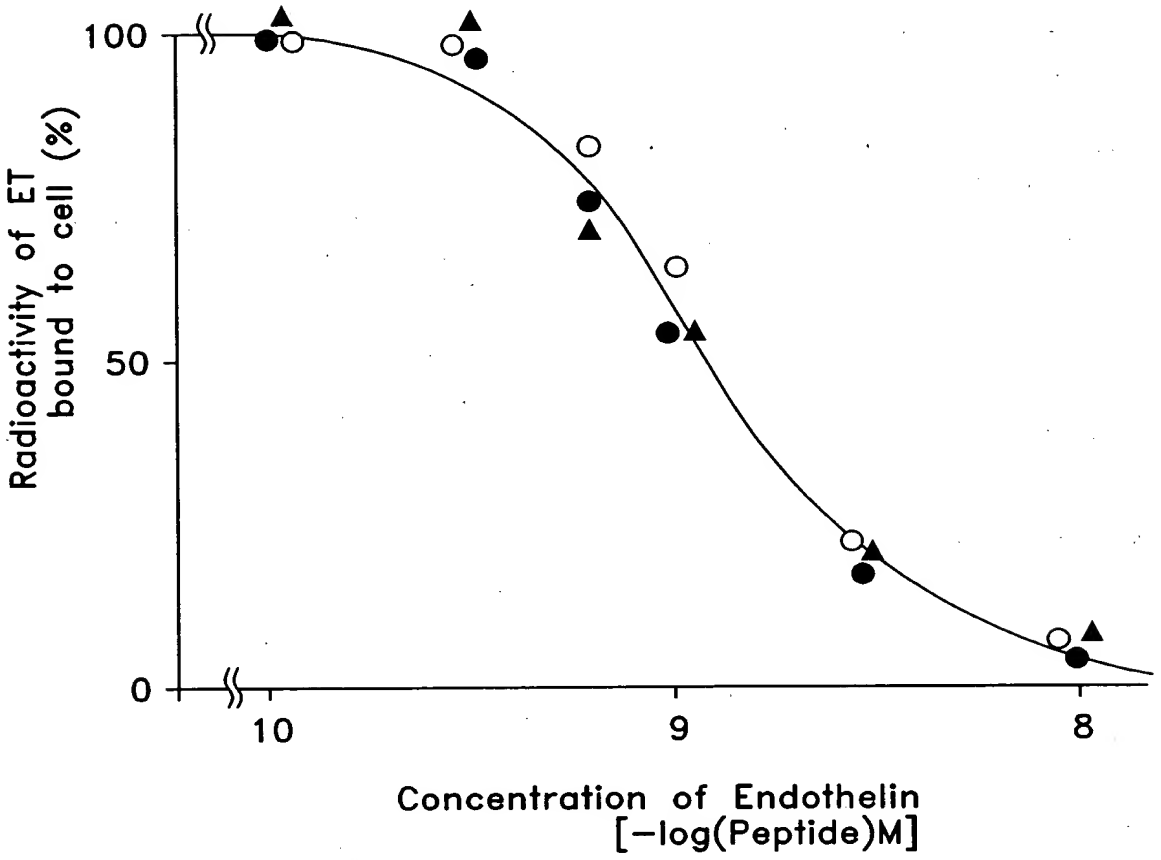
100
50
0
Radioactivity of ET bound to cell (%)
10
9
8
Concentration of Endothelin
[−log(Peptide)M]

Fig. 4

13/16

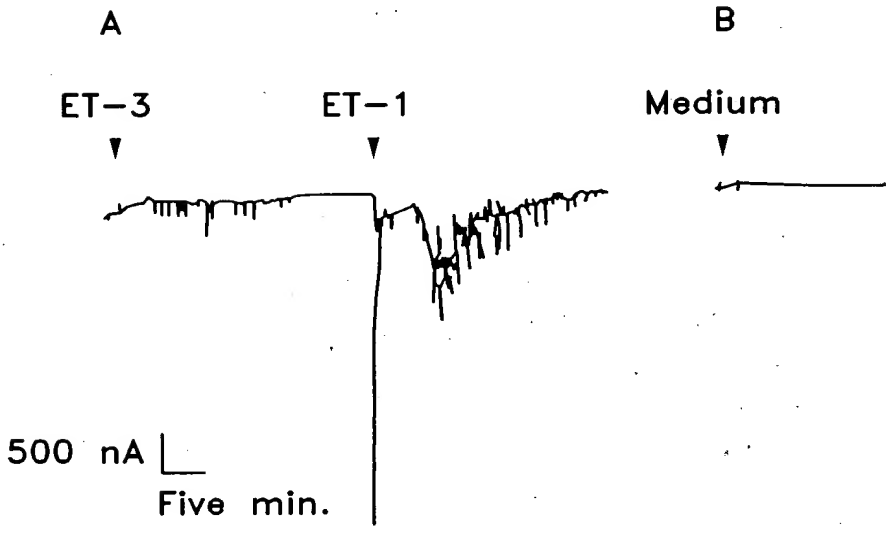

Fig. 5

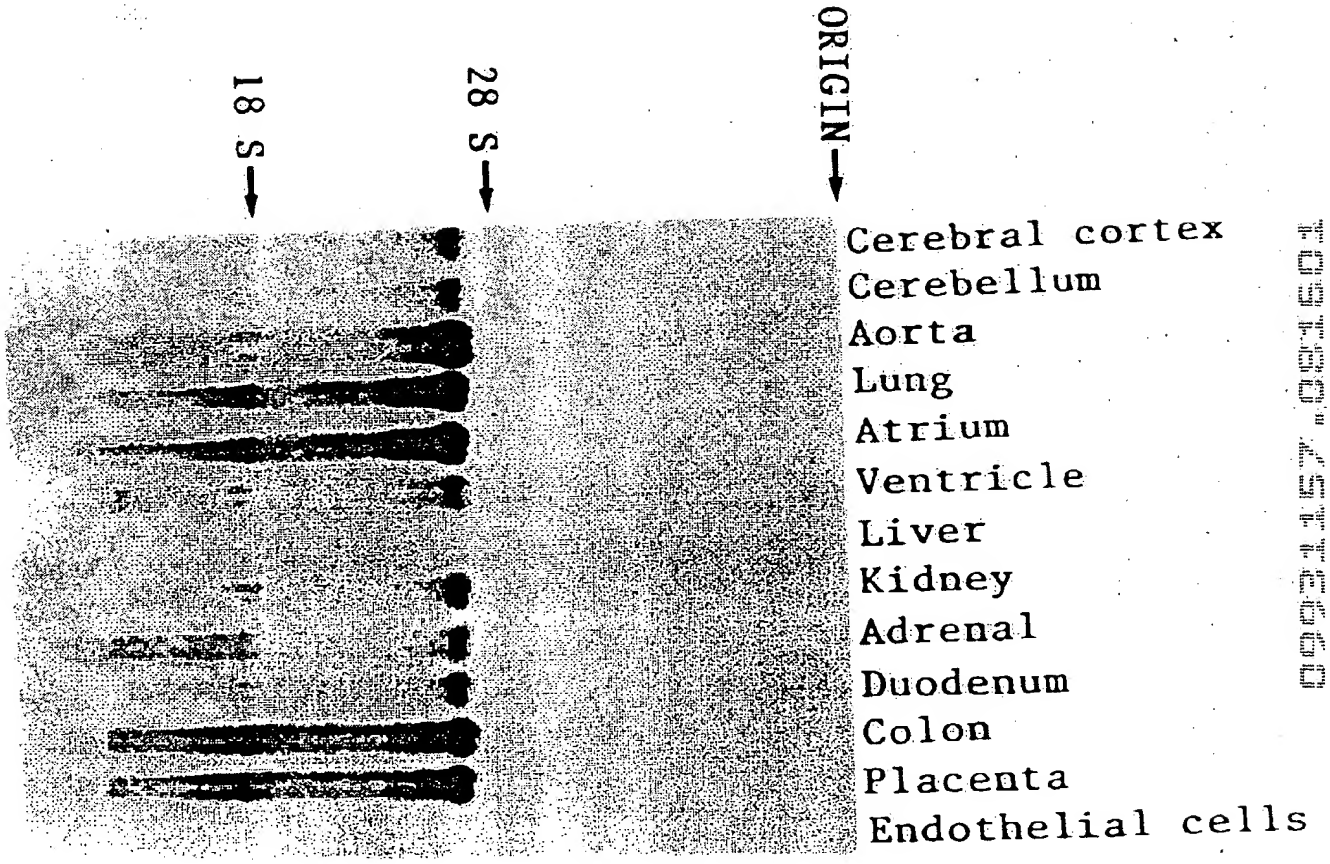
18 S
28 S
ORIGIN
Cerebral cortex
Cerebellum
Aorta
Lung
Atrium
Ventricle
Liver
Kidney
Adrenal
Duodenum
Colon
Placenta
Endothelial cells

Fig. 6

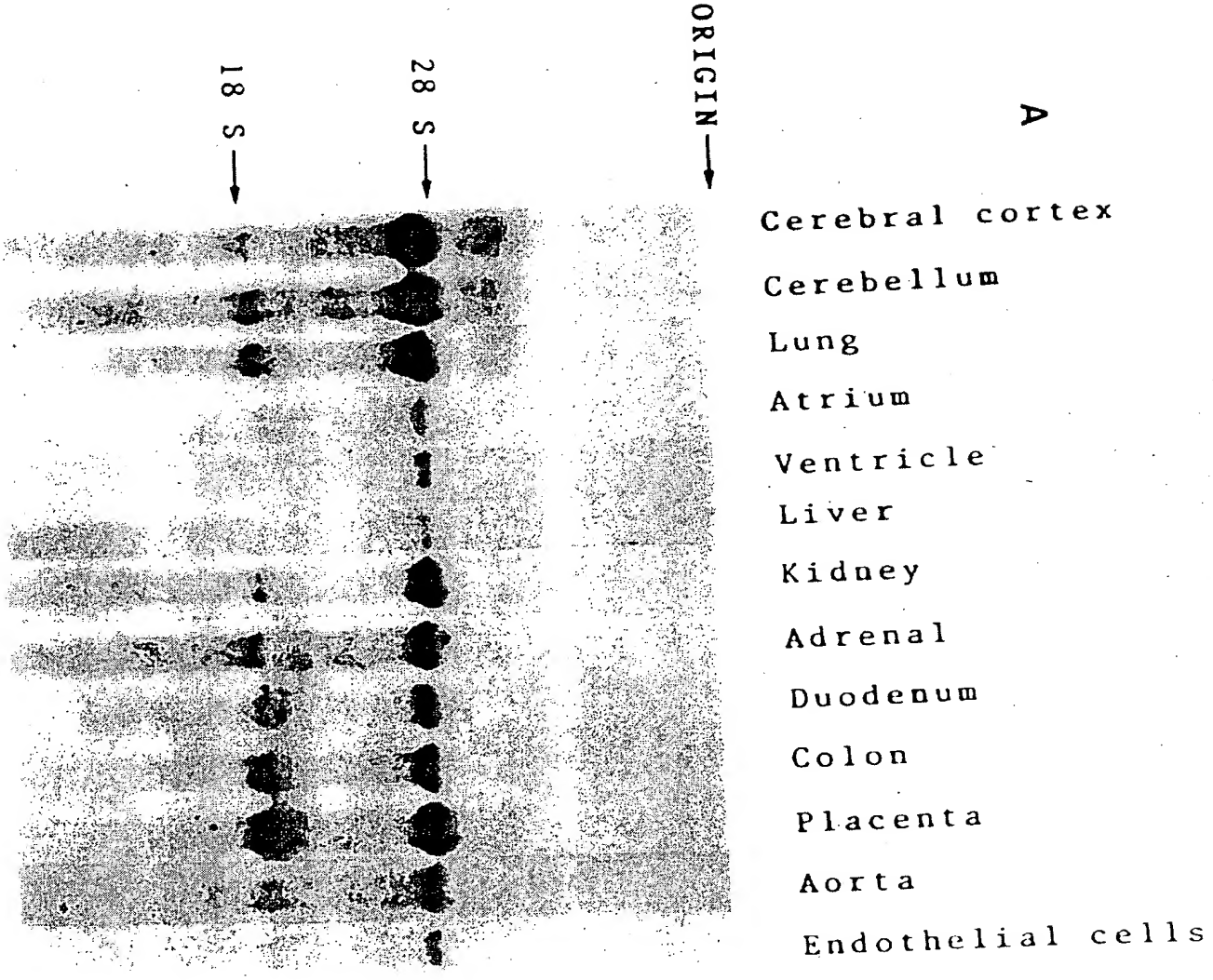
18 S
28 S
ORIGIN
A
Cerebral cortex
Cerebellum
Lung
Atrium
Ventricle
Liver
Kidney
Adrenal
Duodenum
Colon
Placenta
Aorta
Endothelial cells

Fig. 7

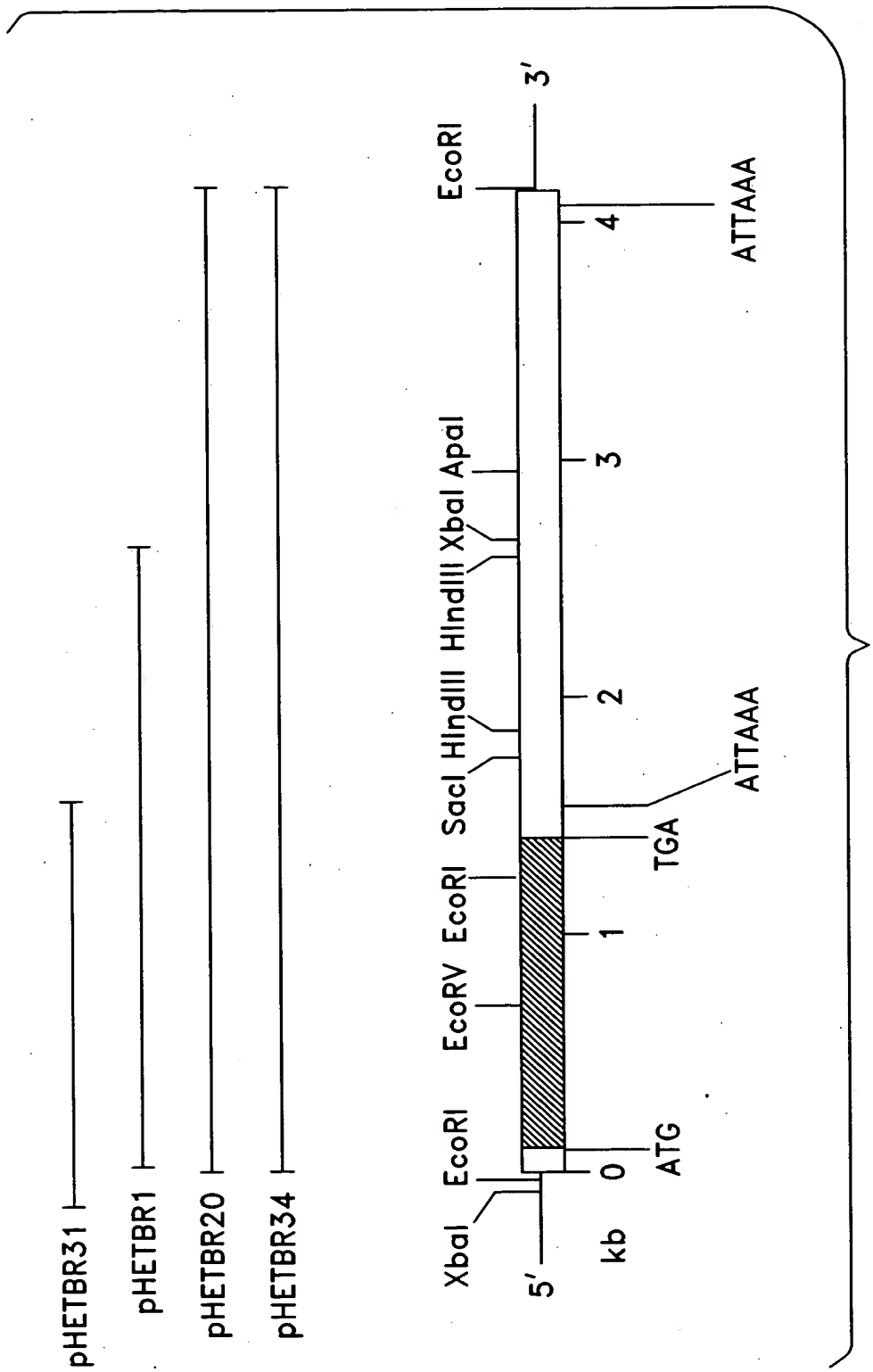
pHETBR31
pHETBR1
pHETBR20
pHETBR34
XbaI
EcoRI
EcoRV
EcoRI
SacI
HindIII
HindIII
XbaI
ApaI
EcoRI
5'
3'
kb
0
1
2
3
4
ATG
TGA
ATTAAA
ATTAAA

Fig. 8